WORKSHOP AGENDA

**"Scaling best practice on integrating DNA fingerprinting of crops into large-scale household surveys"**
Lake Union Conference Room, Bill and Melinda Gates Foundation, Seattle
18th and 19th January 2018

<u>Thurs 18th Jan 2018 – DAY 1</u>

| Time | Topic | Key contributors |
|---|---|---|
| 08:00 | Collect badges<br>Breakfast served | |
| 08:30 | **Introductions, logistics** and a **run-through** of the logic of the program | Richard Caldwell / Chloe Legaspi-Cavin / Phil Pardey /<br>James Stevenson |
| 09:00 | **Overview of pilot efforts to date**<br>Presentation on the >10 pilot studies carried out to date and how they vary methodologically by:<br>• the crop under study (clonal, self, or open-pollinated)<br>• sampling procedure within the plot<br>• types of plant material collected and field protocols for doing so<br>• how the reference library was constructed<br>• how plots that were found to be "mixed" were handled<br>• genetic distance at which two different samples were considered sufficiently similar to be categorized as identical<br>• representativeness of the plots sampled within a country<br><br>Session objective: To highlight and discuss the heterogeneity across the studies, with a view to bringing areas of debate to the forefront | Presentation: James Stevenson (25 mins)<br><br>Additional comments (5 mins each):<br>• Mywish Maredia<br>• Andrzej Kilian<br>• Olaf Erenstein |
| 10:00 | **Stock-take on areas of methodological controversy (PART 1)**<br>Plenary discussion on research design principles that are subject to debate<br><br>Session objective: To generate a list of these areas of concern, and to reach a common understanding that can be born in mind for the rest of the workshop | Discussion led by Phil Pardey |
| 10:45 | Coffee | |
| 11:15 | **Overview of key indicators for which DNA fingerprinting is required**<br>From the perspective of monitoring progress of CGIAR and other research and development institutions, what indicators are we expected to deliver data on? From the perspective of feeding back into the research process, what kinds of question do we need to provide evidence for? | Discussion led by Richard Caldwell |

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Thurs 18th Jan 2018 – DAY 1 CONTINUED

| 11:30 | **Household surveys**<br>Household survey data allow us to measure and answer questions about adoption of improved varieties by farmers and the effects on development outcomes.<br>Taking Ethiopia as an example, we will discuss three archetypal surveys<br>• Nationally-representative panel (approx. 4,000 HHs across ag and non-ag)<br>• Repeated cross-section agricultural survey (>10,000 HHs, ag only)<br>• Single purpose new surveys<br><br>Session objective: To share how the samples and field operations of different kinds of household survey are structured, and how and where DNA fingerprinting can fit in | Presentation: Talip Kilic and Gero Carletto (30 mins)<br><br>Additional comments (5 mins each):<br>• Michael Steiner<br>• Frederic Kosmowski<br>• Olaf Erenstein |
|---|---|---|
| 13:00 | Lunch | |
| 14:00 | **Market / seed system surveys**<br>As improved germplasm makes its way through a seed system involving the CGIAR and other public (national) agencies, private seed companies, agro-dealers and farmer-to-farmer exchanges, there are host of transactions that can influence the identity (and purity) of the varieties under study. For certain research questions we will need to establish a link between what we observe in household surveys and the seed supply chain in a country. Sampling from a seed system perspective is the focus of this session.<br><br>Session objective: Review data requirements for understanding how any of the following – national research programs, private sector seed companies, agrodealers, government agencies, extensionists, and farmers – influence the chain linking varietal releases to what is measured from plant samples taken from farmers' fields. | Presentation: Arturo Silva and Marianne Bänziger (30 mins)<br><br>Additional comments (5 mins each):<br>• Prakash Veettil<br>• Dave Hodson<br>• Leigh Anderson<br>• Travis Lybbert |
| 15:15 | **DNA fingerprinting approaches**<br>The term "DNA fingerprinting" covers a multiplicity of packages of specific laboratory procedures, each with different characteristics and delivering different output.<br><br>Session objective: To review the range of alternative DNA fingerprinting approaches – how they work, their respective strengths and limitations. | Presentation: Kevin Silverstein and Ana Poets (30 mins)<br><br>Additional comments:<br>• Andrzej Kilian; Patrik Stolt (10 mins each)<br>• Tabare Abadie; Rajeev Varshney (5 mins each) |
| 16:30 | Coffee | |
| 17:00 – 18:00 | **Stock-take on areas of methodological controversy (PART 2)**<br>Revisiting the issues from the morning | Marianne Bänziger<br>Karen Macours |

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Fri 19th Jan 2018 – DAY 2

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| 08:00 | Breakfast served | |
| 08:30 | **Recap, and sharing of dinner / breakfast eureka moments** | |
| 08:45 | **Data use, data sharing, data integration, informatics**<br>DNA fingerprinting data has tremendous value. The value of any single dataset is enhanced significantly when it is reconciled with other forms of data from other sources – such as other DNA fingerprinting datasets in other countries, or climate, soils and other data from the same location. There are many obstacles to greater data-sharing and it is not obvious what the correct forum is for facilitating this data integration.<br><br>Session objective: To discuss practical steps to ensure future DNA fingerprinting efforts are set up in such a way that data-sharing and integration are easy | Institutional perspectives (10 – 15 mins each):<br>• Medha Devare (Big Data platform)<br>• Kelly Robbins (Excellence in Breeding platform)<br>• Phil Pardey (G.E.M.S platform)<br><br>Responses (5 – 7 mins each):<br>• Gero Carletto<br>• Greg Traxler |
| 10:00 | **Group work**<br>Self-organization into groups addressing:<br>    a) Reaching consensus on one of the controversies from Day 1, or<br>    b) Prospective research designs addressing specific questions regarding varietal identification / relatedness and purity built around either:<br>        i. Panel survey (4,000 HHs)<br>        ii. Cross-sectional agricultural survey (>10,000 HHs)<br>        iii. New independent bespoke household surveys<br>        iv. Seed system / market-based sampling<br>What kinds of data are needed for which summary statistics? Is it likely to be cost-effective to do it? What kinds of modifications to status quo are needed? What could go wrong?<br>Groups grab coffee whenever suits | |
| 12:15 | **Brief plenary check-in** | |
| 12:30 | Lunch | |
| 13:30 | **Groups continued**, with focus on summarizing key points for guidance document | |
| 14:45 | **Presentations** (5 slides from each group) to plenary | |
| 15:45 | Coffee | |
| 16:00 | **What will it take to scale up DNA fingerprinting for varietal monitoring and make it routine?** Discussion led by Greg Traxler<br>Drawing on the insights from groups, how can we articulate a vision covering:<br>Purpose(s); Scale of coverage; Periodicity; Institutions responsible; Costs and likely sources of funding | |
| 17:15<br>–<br>18:00 | **Discussion on process** Wrap-up led by Karen Macours<br>How to proceed with drafting full document AND<br>Furthering commitment to scaling up in participants' respective institutions | |